



REC'D PCT/PTO 15 DEC 2005

CL2039.ST25
SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company
Hallahan, David L.

<120> CIS-PRENYLTRANSFERASES FROM THE RUBBER-PRODUCING PLANTS RUSSIAN DANDELION (TARAXACUM KOK-SAGHYZ) AND SUNFLOWER (HELIANTHUS ANNUS)

<130> CL2039

<160> 45

<170> PatentIn version 3.1

<210> 1

<211> 746

<212> DNA

<213> Taraxacum kok-saghyz

| | |
|---------------------------------------------------------------------------|-----|
| <400> 1 | 60 |
| gatcgaaggc tttctgaaag aagtttagtataaaaccaa tatggcgtaa gagtcttgg | 60 |
| catcgggtat ctcgataggt tatatgagcc cgtaaggatt gctgctgaga aggccatgga | 120 |
| agccaccgct aaaaactcaa ccacatatct cctcgtatgt gttgcttaca cttcttccca | 180 |
| tgaaatccca cgtgccatcc acgaagctt gtaagaaagc atacgggtca tgaacggaaa | 240 |
| cgggttttc aatggaagcg gatataccaa cgtgaatcat ggaagtcagg cggatcaa | 300 |
| agtgggtggat cttgataagc atatgtacat ggggggtggca ccggatcctg atattttgt | 360 |
| aaggagctcc ggcgaaaccaa ggctgagcaa ctttctgctg tggcagacca ccaactgttt | 420 |
| gttgtattcc ccgaaagctt tgtggccgga gatggggttc tggcaggtgg tttgggaat | 480 |
| cttggagttt caaaaacatt ataattactt ggagaagaag aagaagcagg cgtaaaggatg | 540 |
| tgttcaaaaa gtaaggtaat ctgttttaa atgagttgg agtgtgctgt gagcattaat | 600 |
| gggatttttc ttcccaatataactt gaaacttcaa ttttgggtcg attataatataat atgatccata | 660 |
| tgtatatgaa cgttgtgtga tgcattatac gagcagaaga acgttgtatt tttactaaaa | 720 |
| aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaa | 746 |

<210> 2

CL2039.ST25

<211> 788

<212> DNA

<213> Taraxacum kok-saghyz

| | |
|---------------------------------------------------------------------|-----|
| <400> 2 | |
| gcccttcgcg gatccagacg ctgcgttgc tggcttgat gaaaataatc tattccacca | 60 |
| agttatctct ctctctctct ctctctctct ctctctgtct gtctctcttc | 120 |
| ctctgtctct ctagtataca attggcaaattt aggattaagc cggttcattt gttaaaccaa | 180 |
| gatgcaagtg aatccaatca ttactacaga tagttcactg aaactagtgg aagaagaaag | 240 |
| atcaaatggt aggatcggca atttcttagg aggcttaaac gccaccttaa gaaaactcgt | 300 |
| gtttcgtgtc attgcttctc gccaaatccc agaacacatc gccttcattcc tcgatggaaa | 360 |
| ccgaagggttc gccaggaaat ggaacctcac agaaggcgcc ggccacaaaaa cccgcttcct | 420 |
| agcactcatg tcggtcctca aatactgcta cgagatcggg gtttaagtacg tcaccatcta | 480 |
| cgccttcagc ctcgacaattt tcaatcgacg ccctgatgaa gtccagtacg tcatggactt | 540 |
| gatgcaagac aagatcgaag gcttctgaa agaagtttagt attataaacc aatatggcgt | 600 |
| tagagtcttg ttcatcggtg atctcgatag gttatatgag cccgtaagga ttgctgctga | 660 |
| gaaggccatg gaagccacccg ctaaaaactc aaccacatat ccctcgatgtat gtgtgctta | 720 |
| cacttcttcc catgaaatcc cacgtgccat ccacgaagct tgtgaagaaa gcatacgggt | 780 |
| catgaacg | 788 |

<210> 3

<211> 906

<212> DNA

<213> Taraxacum kok-saghyz

| | |
|-----------------------------------------------------------------------|-----|
| <400> 3 | |
| atgcaagtga atccaatcat tactacagat agttcactga aactagtggaa agaagaaaga | 60 |
| tcaaatggta ggatcggcaa tttcttagga ggcttaaacg ccaccttaag aaaactcgtg | 120 |
| tttcgtgtca ttgcttctcg cccaaatccc gaacacatcg ctttcattcc cgatggaaac | 180 |
| cgaagggttc ccaggaaatg gaacacctaca gaaggcgccg gccacaaaaac cggcttcctta | 240 |
| gcactcatgt cggtcctcaa atactgctac gagatcggag ttaagtacgt caccatctac | 300 |
| gccttcagcc tcgacaattt caatcgacgc cctgatgaaag tccagtacgt catggacttg | 360 |
| atgcaagaca agatcgaagg ctttctgaaa gaagtttagt ttataaaccat atatggcgtt | 420 |
| agagtcttgt tcatcggtga tctcgatagg ttatatgagc ccgttaaggat tgctgctgag | 480 |
| aaggccatgg aagccacccgc taaaaactca accacatatc ccctcgatgtatg tgttgcttac | 540 |

CL2039.ST25

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|
| acttcttccc | atgaaatccc | acgtgccatc | cacgaagctt | gtgaagaaaag | catacgggtc | 600 |
| atgaacggaa | acgggttttt | caatggaaagc | ggatatacca | acgtgaatca | tggaagtcag | 660 |
| gcggtgatca | aagtggtgga | tcttgataag | catatgtaca | tgggggtggc | accggatcct | 720 |
| gatattttag | taaggagctc | cggcggaaaca | aggctgagca | actttctgct | gtggcagacc | 780 |
| accaactgtt | tgttgattc | cccgaaagct | ttgtggccgg | agatggggtt | ctggcaggtg | 840 |
| gtttggggaa | tcttgagtt | tcaaaacaat | tataattact | tggagaagaa | gaagaagcag | 900 |
| gcgtaa | | | | | | 906 |

<210> 4

<211> 301

<212> PRT

<213> Taraxacum kok-saghyz

<400> 4

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Val | Asn | Pro | Ile | Ile | Thr | Thr | Asp | Ser | Ser | Leu | Lys | Leu | Val |
| 1 | | | | | 5 | | | | 10 | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Glu | Arg | Ser | Asn | Gly | Arg | Ile | Gly | Asn | Phe | Leu | Gly | Gly | Leu |
| | | | | | | | | 20 | 25 | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ala | Thr | Leu | Arg | Lys | Leu | Val | Phe | Arg | Val | Ile | Ala | Ser | Arg | Pro |
| | | | | | | | 35 | 40 | | | 45 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Glu | His | Ile | Ala | Phe | Ile | Leu | Asp | Gly | Asn | Arg | Arg | Phe | Ala |
| | | | | | | | 50 | 55 | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Trp | Asn | Leu | Thr | Glu | Gly | Ala | Gly | His | Lys | Thr | Gly | Phe | Leu |
| | | | | | | 65 | 70 | | 75 | | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Leu | Met | Ser | Val | Leu | Lys | Tyr | Cys | Tyr | Glu | Ile | Gly | Val | Lys | Tyr |
| | | | | | | | 85 | | 90 | | 95 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Ile | Tyr | Ala | Phe | Ser | Leu | Asp | Asn | Phe | Asn | Arg | Arg | Pro | Asp |
| | | | | | | | 100 | 105 | | | 110 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Tyr | Val | Met | Asp | Leu | Met | Gln | Asp | Lys | Ile | Glu | Gly | Phe |
| | | | | | | | 115 | 120 | | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Lys | Glu | Val | Ser | Ile | Ile | Asn | Gln | Tyr | Gly | Val | Arg | Val | Leu | Phe |
| | | | | | | | 130 | | 135 | | 140 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gly | Asp | Leu | Asp | Arg | Leu | Tyr | Glu | Pro | Val | Arg | Ile | Ala | Ala | Glu |
| | | | | | | | 145 | | 150 | | 155 | | 160 | | |

CL2039.ST25

Lys Ala Met Glu Ala Thr Ala Lys Asn Ser Thr Thr Tyr Leu Leu Val
165 170 175

Cys Val Ala Tyr Thr Ser Ser His Glu Ile Pro Arg Ala Ile His Glu
180 185 190

Ala Cys Glu Glu Ser Ile Arg Val Met Asn Gly Asn Gly Phe Phe Asn
195 200 205

Gly Ser Gly Tyr Thr Asn Val Asn His Gly Ser Gln Ala Val Ile Lys
210 215 220

Val Val Asp Leu Asp Lys His Met Tyr Met Gly Val Ala Pro Asp Pro
225 230 235 240

Asp Ile Leu Val Arg Ser Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu
245 250 255

Leu Trp Gln Thr Thr Asn Cys Leu Leu Tyr Ser Pro Lys Ala Leu Trp
260 265 270

Pro Glu Met Gly Phe Trp Gln Val Val Trp Gly Ile Leu Glu Phe Gln
275 280 285

Asn Asn Tyr Asn Tyr Leu Glu Lys Lys Lys Lys Gln Ala
290 295 300

<210> 5

<211> 505

<212> DNA

<213> Helianthus annus

| | | |
|--------------------------------------------------------------------|-----|--|
| <400> 5 | | |
| accagaaaaga ttgaagggtt tatgaaagaa ttaacaattg tgaacaggta tggtgttaga | 60 | |
| gtcttgttta tcggcgatct taaaaggtta tacgagcccg ttagagttgc agccgagaaa | 120 | |
| gcaatggagg ccactgctaa caacacacat acatatctt tagtatgtgt tgcttacact | 180 | |
| tcttcacacg aaatcccgcg tgccgttat gaatcttgcg aagaaaagag tggtggaacc | 240 | |
| ggagttatga ttaatggaaa tggaagtgtg aacggagatt acagtgaaga aaagagtgg | 300 | |
| ggaaccggag ttatggtaa tggaaatggg agtgtgaatg gagattacag taatggagat | 360 | |
| catgaggagg gggtaaagt ggtggatatt gacaaacata tgtatatggc agtggctcct | 420 | |
| gatcctgata tttggtcag gagctcaggg gagacgaggt ttagtaactt tttgctgtgg | 480 | |
| caaaccacca actgcgtgtt gtatt | 505 | |

<210> 6

<211> 168

<212> PRT

<213> *Helianthus annus*

<400> 6

Thr Arg Lys Ile Glu Gly Phe Met Lys Glu Leu Thr Ile Val Asn Arg
 1 5 10 15

Tyr Gly Val Arg Val Leu Phe Ile Gly Asp Leu Lys Arg Leu Tyr Glu
 20 25 30

Pro Val Arg Val Ala Ala Glu Lys Ala Met Glu Ala Thr Ala Asn Asn
 35 40 45

Thr His Thr Tyr Leu Leu Val Cys Val Ala Tyr Thr Ser Ser His Glu
 50 55 60

Ile Pro Arg Ala Val Tyr Glu Ser Cys Glu Glu Lys Ser Gly Gly Thr
 65 70 75 80

Gly Val Met Ile Asn Gly Asn Gly Ser Val Asn Gly Asp Tyr Ser Glu
 85 90 95

Glu Lys Ser Gly Gly Thr Gly Val Met Val Asn Gly Asn Gly Ser Val
 100 105 110

Asn Gly Asp Tyr Ser Asn Gly Asp His Glu Glu Gly Val Lys Val Val
 115 120 125

Asp Ile Asp Lys His Met Tyr Met Ala Val Ala Pro Asp Pro Asp Ile
 130 135 140

Leu Val Arg Ser Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp
 145 150 155 160

Gln Thr Thr Asn Cys Val Leu Tyr
 165

<210> 7

<211> 228

<212> PRT

<213> *Calendula officinalis*

<400> 7

CL2039.ST25

Met Pro Lys His Val Ala Phe Ile Met Asp Gly Asn Arg Arg Trp Ala
 1 5 10 15

Val Glu Lys Gly Trp Ser Pro Met Thr Gly His Ser Ala Met Arg Lys
 20 25 30

Thr Leu Gln Ser Leu Leu Phe Arg Cys Ser Lys Phe Lys Ile Lys Ala
 35 40 45

Val Ser Ile Tyr Ala Phe Ser Thr Glu Asn Trp Thr Arg Pro Lys Glu
 50 55 60

Glu Val Asp Phe Leu Met Glu Met Tyr Glu Asp Leu Leu Arg Thr Asp
 65 70 75 80

Ala Glu Glu Leu Leu Ser Leu Gly Cys Arg Val Ser Ile Met Gly Lys
 85 90 95

Lys Thr Asn Leu Pro Lys Ser Leu Gln Lys Leu Cys Ile Glu Ile Glu
 100 105 110

Glu Lys Ser Arg Ala Asn Ser Gly Thr His Val Asn Tyr Ala Leu Asn
 115 120 125

Tyr Ser Gly Lys Tyr Asp Ile Ile Glu Ala Cys Lys Ser Val Ala Thr
 130 135 140

Lys Val Lys Asp Gly Val Ile Ile Pro Lys Gln Ile Asp Glu Lys Tyr
 145 150 155 160

Phe Lys Gln Glu Leu Gly Thr Lys Met Ile Asp Phe Pro Tyr Pro Asp
 165 170 175

Leu Val Ile Arg Thr Ser Gly Glu Ile Arg Leu Ser Asn Phe Met Leu
 180 185 190

Trp Gln Met Ala Tyr Ser Glu Leu Tyr Phe Thr Asp Lys Tyr Phe Pro
 195 200 205

Asp Phe Gly Glu Asn Asp Leu Ile Glu Ala Leu Leu Ala Phe Gln Lys
 210 215 220

Val Arg Lys Cys
 225

<210> 8

<211> 290

<212> PRT

<213> Hevea brasiliensis

<400> 8

Met Glu Leu Tyr Asn Gly Glu Arg Pro Ser Val Phe Arg Leu Leu Gly
 1 5 10 15

Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
 20 25 30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
 35 40 45

Lys His Lys Leu Pro Glu Gly Gly His Lys Ala Gly Phe Leu Ala
 50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
 65 70 75 80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
 85 90 95

Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
 100 105 110

Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
 115 120 125

Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
 130 135 140

Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
 145 150 155 160

Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
 165 170 175

Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
 180 185 190

Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
 195 200 205

Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
 210 215 220

Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
 225 230 235 240

Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
 245 250 255

CL2039.ST25

Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
260 265 270

Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
275 280 285

Leu Lys
290

<210> 9

<211> 290

<212> PRT

<213> **Hevea brasiliensis**

<400> 9

Met Glu Leu Tyr Asn Gly Glu Arg Pro Ser Val Phe Arg Leu Leu Glu
1 5 10 15

Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
20 25 30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
35 40 45

Lys His Lys Leu Pro Glu Gly Gly His Lys Ala Gly Phe Leu Ala
50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
65 70 75 80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
85 90 95

Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
100 105 110

Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
115 120 125

Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
130 135 140

Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
145 150 155 160

Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
Page 8

CL2039.ST25

165

170

175

Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
180 185 190

Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
195 200 205

Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
210 215 220

Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
225 230 235 240

Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
245 250 255

Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
260 265 270

Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
275 280 285

Leu Lys
290

<210> 10

<211> 296

<212> PRT

<213> **Hevea brasiliensis**

<400> 10

Met Glu Ile Tyr Thr Gly Gln Arg Pro Ser Val Phe Arg Ile Phe Gly
1 5 10 15

Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
20 25 30

Pro Thr His Leu Ala Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Lys
35 40 45

Lys His Lys Met Lys Glu Ala Glu Gly Tyr Lys Ala Gly Tyr Leu Ala
50 55 60

Leu Leu Arg Thr Leu Thr Tyr Cys Tyr Glu Leu Gly Val Arg Tyr Val
65 70 75 80

CL2039.ST25

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Gln Pro Arg Glu
 85 90 95

Val Gln Cys Val Met Asn Leu Met Met Glu Lys Ile Glu Glu Ile Ile
 100 105 110

Val Glu Glu Ser Ile Met Asn Ala Tyr Asp Val Gly Val Arg Ile Val
 115 120 125

Gly Asn Leu Asn Leu Leu Asp Glu Pro Ile Arg Ile Ala Ala Glu Lys
 130 135 140

Ile Met Arg Ala Thr Ala Asn Asn Ser Gly Phe Val Leu Leu Ile Ala
 145 150 155 160

Val Ala Tyr Ser Ser Thr Asp Glu Ile Gly His Ala Val Glu Glu Ser
 165 170 175

Ser Lys Asp Lys Leu Asn Ser Asn Glu Val Cys Asn Asn Gly Ile Glu
 180 185 190

Ala Glu Gln Glu Phe Lys Glu Ala Asn Gly Thr Gly Asn Ser Val Ile
 195 200 205

Pro Val Gln Lys Thr Glu Ser Tyr Ser Gly Ile Asn Leu Ala Asp Leu
 210 215 220

Glu Lys Asn Thr Tyr Val Asn Pro His Pro Asp Val Leu Ile Arg Thr
 225 230 235 240

Ser Gly Leu Ser Arg Leu Ser Asn Tyr Leu Leu Trp Gln Thr Ser Asn
 245 250 255

Cys Ile Leu Tyr Ser Pro Phe Ala Leu Trp Pro Glu Ile Gly Leu Arg
 260 265 270

His Leu Val Trp Thr Val Met Asn Phe Gln Arg His His Ser Tyr Leu
 275 280 285

Glu Lys His Lys Glu Tyr Leu Lys
 290 295

<210> 11

<211> 309

<212> PRT

<213> Vitis sp.

<400> 11

CL2039.ST25

Met Leu Ser Phe Arg Phe Pro Ile Ser Ala Asp Asn Ala Arg His Thr
1 5 10 15

Phe Lys Ser Lys His Ser Ser Cys Thr Phe Arg Ser Asn Arg Ile Asp
20 25 30

Ser Phe Ser Phe Pro Pro Ile Ser Val Pro Arg Phe His Lys Leu Arg
35 40 45

Thr Ala Lys Thr Asp Val Val Gly Glu Glu Glu Ala Arg Glu Val Asn
50 55 60

Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro
65 70 75 80

Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys
85 90 95

Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu
100 105 110

Arg Glu Leu Val Glu Leu Cys Cys Lys Trp Gly Ile Lys Val Leu Ser
115 120 125

Val Phe Ala Phe Ser Tyr Asp Asn Trp Ser Arg Ser Glu Gly Glu Val
130 135 140

Gly Phe Leu Met Ser Leu Ile Glu Arg Val Val Lys Ala Glu Leu Pro
145 150 155 160

Ile Leu Gly Gly Lys Ala Phe Glu Cys Arg Asp Trp Gly Phe Val Lys
165 170 175

Ala Ser Glu Gln Leu Gln Leu Ile Ile Asp Val Glu Glu Thr Thr Lys
180 185 190

Glu Asn Ser Arg Leu Gln Phe Ile Val Ala Leu Ser Tyr Ser Gly Gln
195 200 205

Cys Asp Ile Leu Gln Ala Cys Lys Asn Ile Gly His Lys Val Lys Asp
210 215 220

Gly Leu Ile Glu Pro Glu Asp Ile Asn Lys Ser Leu Ile Glu Gln Glu
225 230 235 240

Leu Gln Thr Asn Cys Thr Glu Phe Pro Phe Pro Asp Leu Leu Ile Arg
245 250 255

Thr Ser Gly Glu Leu Arg Val Ser Asn Phe Met Leu Trp Gln Ile Ala
260 265 270

CL2039.ST25

Tyr Thr Glu Leu Cys Phe Phe Ser Thr Leu Trp Pro Asp Phe Gly Lys
275 280 285

Asp Glu Phe Val Glu Ala Leu Ser Ser Phe Gln Lys Arg Gln Arg Arg
290 295 300

Tyr Gly Gly Arg Asn
305

<210> 12

<211> 252

<212> PRT

<213> Oryza sativa

<400> 12

Met Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala
1 5 10 15

Lys Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser
20 25 30

Ala Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr
35 40 45

Ile Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr
50 55 60

Glu Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu
65 70 75 80

Leu Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe
85 90 95

Trp Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu
100 105 110

Lys Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val
115 120 125

Cys Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys
130 135 140

Val Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser
145 150 155 160

Val Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp
Page 12

165

CL2039.ST25
170

175

Arg His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg
180 185 190

Thr Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr
195 200 205

Phe Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe
210 215 220

Lys His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser
225 230 235 240

Ile Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
245 250

<210> 13

<211> 299

<212> PRT

<213> Oryza sativa

<400> 13

Met Leu Gly Ser Leu Met Ser Tyr Leu Pro Ser Val Asp Ser Lys Thr
1 5 10 15

Glu Asn Thr Asp Glu Leu Ile Ala Thr Gly Val Leu Ala Ser Leu Gln
20 25 30

Asn Phe Ile Arg Lys Cys Ile Val Ala Val Leu Ser Tyr Gly Pro Met
35 40 45

Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala Lys
50 55 60

Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser Ala
65 70 75 80

Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr Ile
85 90 95

Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr Glu
100 105 110

Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu Leu
115 120 125

CL2039.ST25

Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe Trp
 130 135 140

Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu Lys
 145 150 155 160

Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val Cys
 165 170 175

Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys Val
 180 185 190

Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser Val
 195 200 205

Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp Arg
 210 215 220

His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg Thr
 225 230 235 240

Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr Phe
 245 250 255

Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe Lys
 260 265 270

His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser Ile
 275 280 285

Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
 290 295

<210> 14

<211> 322

<212> PRT

<213> Glycine max

<400> 14

Met Phe Ser Leu Arg Leu Pro Ile Pro Leu Val Lys Thr Pro Pro Ser
 1 5 10 15

Pro Ser Cys Tyr Tyr Ser His Tyr Tyr His Tyr Arg Tyr Arg Tyr Arg
 20 25 30

Cys Tyr His Pro Phe His His Arg Ser Gln Thr Gln Ser Leu Ile Val
 35 40 45

CL2039.ST25

Ser Lys Arg Gly Ser Ala Ile Ala Lys Cys His Ala Asp Ser Val Thr
50 55 60

Leu Arg Asp Asp Gly Val Ser Leu Ala Gln Glu Ser Leu Glu Pro Leu
65 70 75 80

Pro Ala Glu Leu Ala Ala Glu Met Met Pro Lys His Val Ala Val Ile
85 90 95

Met Asp Gly Asn Gly Arg Trp Ala Lys Val Lys Gly Leu Pro Pro Ser
100 105 110

Ala Gly His Gln Ala Gly Val Gln Ser Leu Arg Lys Met Val Arg Leu
115 120 125

Cys Cys Ser Trp Gly Ile Lys Val Leu Thr Val Phe Ala Phe Ser Thr
130 135 140

Asp Asn Trp Val Arg Pro Lys Val Glu Val Asp Phe Leu Met Arg Leu
145 150 155 160

Phe Glu Arg Thr Ile Asn Ser Glu Val Gln Thr Phe Lys Arg Glu Gly
165 170 175

Ile Arg Ile Ser Val Ile Gly Asp Ser Ser Arg Leu Pro Glu Ser Leu
180 185 190

Lys Arg Met Ile Ala Ser Ala Glu Glu Asp Thr Lys Gln Asn Ser Arg
195 200 205

Phe Gln Leu Ile Val Ala Val Gly Tyr Ser Gly Lys Tyr Asp Val Val
210 215 220

Gln Ala Cys Lys Ser Val Ala Lys Lys Val Lys Asp Gly His Ile His
225 230 235 240

Leu Asp Asp Ile Asn Glu Asn Ile Ile Glu Gln Glu Leu Glu Thr Asn
245 250 255

Cys Thr Glu Phe Pro Tyr Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
260 265 270

Leu Arg Val Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Thr Glu Leu
275 280 285

Tyr Phe Asn Arg Glu Leu Trp Pro Asp Phe Gly Lys Asp Glu Phe Val
290 295 300

Asp Ala Leu Ser Ser Phe Gln Gln Arg Gln Arg Arg Tyr Gly Gly Arg
305 310 315 320

His Ser

<210> 15

<211> 266

<212> PRT

<213> *Triticum aestivum*

<400> 15

Met Pro Leu Ser Asn Ser Thr Ser Ser Val Pro Ala Val Thr Val Pro
1 5 10 15Ala Ala Glu Glu Leu Leu Ser Gln Gly Leu Arg Ala Glu Ser Leu Pro
20 25 30Arg His Val Ala Leu Val Met Asp Gly Asn Ser Arg Trp Ala Ala Ala
35 40 45Arg Gly Leu Pro Pro Thr Asp Gly His Glu His Gly Met Arg Ala Leu
50 55 60Met Arg Thr Val Arg Leu Ser Arg Ala Trp Gly Ile Arg Val Leu Thr
65 70 75 80Ala Phe Gly Phe Ser Leu Glu Asn Trp Asn Arg Pro Lys Ala Glu Val
85 90 95Asp Phe Leu Met Ala Leu Ile Glu Arg Phe Ile Asn Asp Asn Leu Ala
100 105 110Glu Phe Leu Arg Glu Gly Thr Arg Leu Arg Ile Ile Gly Asp Arg Ser
115 120 125Arg Leu Pro Ile Ser Val Gln Lys Thr Ala Arg Asp Ala Glu Glu Ala
130 135 140Thr Arg Asn Asn Ser Gln Leu Asp Leu Val Leu Ala Ile Ser Tyr Ser
145 150 155 160Gly Arg Met Asp Ile Val Gln Ala Cys Arg Asn Leu Ala Gln Lys Val
165 170 175Asp Ala Lys Leu Leu Arg Pro Glu Asp Ile Asp Glu Ser Leu Phe Ala
180 185 190Asp Glu Leu Gln Thr Ser Glu Thr Ser Cys Pro Asp Leu Leu Ile Arg
Page 16

195

200

205

Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Leu Trp Gln Ser Ala
 210 215 220

Tyr Ser Glu Leu Phe Phe Thr Asp Thr Leu Trp Pro Asp Phe Gly Glu
 225 230 235 240

Ala Gln Tyr Leu Gln Ala Met Met Ala Phe Gln Ser Arg Asp Arg Arg
 245 250 255

Phe Gly Arg Arg Lys Asn Asn Ala Ala Leu
 260 265

<210> 16

<211> 287

<212> PRT

<213> Dimorphotheca sinuata

<400> 16

Met Leu Asn Leu Pro Leu Tyr Leu Pro Lys Tyr Pro Cys Tyr Phe Pro
 1 5 10 15

Ala Ser Leu Ser Thr Asn His His Arg Gly Leu Tyr Val Phe Asn Gln
 20 25 30

Ser Asp Thr Thr Gly Gly Ile Asn Ser Leu Glu Glu Arg Ile Thr
 35 40 45

Pro Ala Gly Leu Lys His Glu Leu Met Pro Lys His Val Ala Val Ile
 50 55 60

Met Asp Gly Asn Arg Arg Trp Ala Arg Ser Arg Gly Leu Met Pro Asp
 65 70 75 80

Ala Gly Tyr Met Glu Gly Ala Arg Ser Leu Lys Val Met Val Glu Leu
 85 90 95

Cys Arg Lys Trp Gly Ile Gln Val Leu Thr Val Phe Ala Phe Ser Ala
 100 105 110

Asp Asn Trp Leu Arg Pro Lys Val Glu Val Asp Phe Leu Met Gly Leu
 115 120 125

Ile Glu Ser Val Leu Lys Asp Glu Val Val His Met Ile Lys Glu Gly
 130 135 140

CL2039.ST25

Ile Gln Leu Ser Val Ile Gly Asp Thr Ser Lys Leu Pro Lys Ser Val
 145 150 155 160

Lys Arg Ile Ile Thr Tyr Ala Glu Asn Ile Thr Lys Asn Asn Ser Gln
 165 170 175

Leu Asn Leu Val Val Ala Ile Asn Tyr Ser Gly Lys Tyr Asp Ile Val
 180 185 190

Gln Ala Cys Gln Ser Ile Ala Leu Lys Val Lys Asp Gly Val Ile Gln
 195 200 205

Pro Glu Glu Ile Asn Glu Phe Thr Ile Glu Asn Glu Leu Gly Thr Asn
 210 215 220

Cys Ile Pro Phe Pro His Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
 225 230 235 240

Leu Arg Val Ser Asn Phe Phe Leu Trp Gln Leu Ala Tyr Thr Glu Leu
 245 250 255

Tyr Phe Ser Glu Thr Leu Trp Pro Asp Phe Gly Glu Asp Glu Leu Leu
 260 265 270

His Ala Leu Asn Thr Phe Gln His Arg Arg Arg Tyr Gly Gly
 275 280 285

<210> 17

<211> 750

<212> DNA

<213> *Micrococcus luteus*

<300>

<301> Shimizu,N., Koyama,T. and Ogura,K.

<302> Molecular Cloning, Expression, and Purification of Undecaprenyl Diphosphate Synthase: No Sequence Similarity between E- and Z-prenyl Diphosphate Synthases

<303> J. Biol. Chem.

<304> 273

<305> 31

<306> 19476-19481

<307> 1998-07-31

<308> AB004319

<309> 1997-05-29

CL2039.ST25

<400> 17
 atgtttccaa ttaagaagcg aaaagcaata aaaaataata acattaatgc ggcacaatt 60
 ccgaaacata ttgcaatcat tatggacgga aatggccgat gggcaaaaca gaaaaaaatg 120
 ccgcgcataa aaggacatta tgaaggcatg cagaccgtaa agaaaatcac aagatatgct 180
 agtgatttag gtgtaaagta cttaacgctg tacgcatttt caactgaaaa ttggtctcg 240
 cctaaagatg aggttaatta cttgatgaaa ctaccgggtg attttttaaa cacatttta 300
 ccggaactca ttgaaaaaaaaa tgttaaagtt gaaacgattg gctttattga tgatttaccg 360
 gaccatacaa aaaaagcagt gttagaagcg aaagagaaaa ccaaacataa tacaggttt 420
 acgctcgtgt ttgcactgaa ttatggtgg cgtaaagaaa ttatttcagc agtgcagtta 480
 atcgcagagc gttacaaatc tggtgaaatt tcttttagatg aaatttagtga aactcatttt 540
 aatgaatatt tatttacagc aaatatgcct gatcctgagt tgttaatcag aacttccggt 600
 gaagaacgtt taagtaactt tttaatttgg caatgttcat atagtgagtt tgtatttata 660
 gatgaattct ggccggattt taatgaagaa agtttagcac aatgtatatc aatatatcag 720
 aatcgtcatac gacgttttgg tggattataa 750

<210> 18

<211> 249

<212> PRT

<213> *Micrococcus luteus*

<400> 18

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Pro | Ile | Lys | Lys | Arg | Lys | Ala | Ile | Lys | Asn | Asn | Asn | Ile | Asn |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Gln | Ile | Pro | Lys | His | Ile | Ala | Ile | Ile | Met | Asp | Gly | Asn | Gly |
| | | | | 20 | | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Trp | Ala | Lys | Gln | Lys | Lys | Met | Pro | Arg | Ile | Lys | Gly | His | Tyr | Glu |
| | | | | 35 | | | 40 | | | | 45 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Met | Gln | Thr | Val | Lys | Lys | Ile | Thr | Arg | Tyr | Ala | Ser | Asp | Leu | Gly |
| | | | | 50 | | | 55 | | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Tyr | Leu | Thr | Leu | Tyr | Ala | Phe | Ser | Thr | Glu | Asn | Trp | Ser | Arg |
| 65 | | | | 70 | | | | 75 | | | 80 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Asp | Glu | Val | Asn | Tyr | Leu | Met | Lys | Leu | Pro | Gly | Asp | Phe | Leu |
| | | | | 85 | | | | 90 | | | 95 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Thr | Phe | Leu | Pro | Glu | Leu | Ile | Glu | Lys | Asn | Val | Lys | Val | Glu | Thr |
| | | | | | | | | | | | | | | | |

CL2039.ST25

| | | | |
|-----------------------------------------------------------------|-----|-----|-----|
| 100 | 105 | 110 | |
| Ile Gly Phe Ile Asp Asp Leu Pro Asp His Thr Lys Lys Ala Val Leu | | | |
| 115 | 120 | 125 | |
| Glu Ala Lys Glu Lys Thr Lys His Asn Thr Gly Leu Thr Leu Val Phe | | | |
| 130 | 135 | 140 | |
| Ala Leu Asn Tyr Gly Gly Arg Lys Glu Ile Ile Ser Ala Val Gln Leu | | | |
| 145 | 150 | 155 | 160 |
| Ile Ala Glu Arg Tyr Lys Ser Gly Glu Ile Ser Leu Asp Glu Ile Ser | | | |
| 165 | 170 | 175 | |
| Glu Thr His Phe Asn Glu Tyr Leu Phe Thr Ala Asn Met Pro Asp Pro | | | |
| 180 | 185 | 190 | |
| Glu Leu Leu Ile Arg Thr Ser Gly Glu Glu Arg Leu Ser Asn Phe Leu | | | |
| 195 | 200 | 205 | |
| Ile Trp Gln Cys Ser Tyr Ser Glu Phe Val Phe Ile Asp Glu Phe Trp | | | |
| 210 | 215 | 220 | |
| Pro Asp Phe Asn Glu Glu Ser Leu Ala Gln Cys Ile Ser Ile Tyr Gln | | | |
| 225 | 230 | 235 | 240 |
| Asn Arg His Arg Arg Phe Gly Gly Leu | | | |
| 245 | | | |

<210> 19
 <211> 861
 <212> DNA
 <213> *Saccharomyces cerevisiae*

| | |
|-------------------------------------------------------------------|-----|
| <400> 19 | 60 |
| atggaaacgg atagtggat acctggcat tcatttgtgt taaagtggac aaaaaacatc | 60 |
| tttgcgcga cattgcgtgc atctaactgt gtacctagac atgttgggtt catcatggat | 120 |
| ggAACAGGA GATTGCGTAG AAAGAAAGAG ATGGACGTAAG AGGAGGGCCA CGAGGCAGGA | 180 |
| TTTGTAGTA TGAGTAGAAT CTTAGAACTG TGTATGAAG CAGGAGTCGA TACGGCTACC | 240 |
| GTGTTGCCT TTTCAATTGA AAATTCAAG AGGAGCTCAC GGAAAGTTGA ATCACTGATG | 300 |
| ACTTTAGCGC GCGAAAGGAT ACGACAAATC ACAGAACGTG GAGAGCTGGC CTGTAAGTAT | 360 |
| GGGGTACGCA TTAAAATTAT CGGCATCTC TCTTGTGG ATAAGTCTCT ATTAGAAGAT | 420 |
| GTTCGGGTTG CTGTGAAAC TACAAAGAAC AACAAAAGGG CCACGTTAAA TATCTGTTT | 480 |
| CCATATACAG GCAGGGAAGA AATCTGCAT GCCATGAAAG AAACAATTGT TCAACATAAG | 540 |

CL2039.ST25

| | |
|------------------------------------------------------------------|-----|
| aaggcgccg ctatagacga aagcacgtta gaatcgcatc tctacacggc ggggttaccc | 600 |
| ccttagatt tattgattag gacaagtggc gtttccagat taagtgactt tttgatatgg | 660 |
| caggcatcga gtaagggcgt acgcatcgaa ttgctggatt gtttatggcc agagtttgg | 720 |
| cctatacgga tggcatggat tttattaaaa tttcgttcc acaaatcctt ttaaaca | 780 |
| gagtacagat tagaggaagg tgattatgac gagaaacca atggggaccc catcgattt | 840 |
| aaagaaaaaa agttgaatta a | 861 |

<210> 20

<211> 286

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 20

| | |
|-----------------------------------------------------------------|--|
| Met Glu Thr Asp Ser Gly Ile Pro Gly His Ser Phe Val Leu Lys Trp | |
| 1 5 10 15 | |

| | |
|-----------------------------------------------------------------|--|
| Thr Lys Asn Ile Phe Ser Arg Thr Leu Arg Ala Ser Asn Cys Val Pro | |
| 20 25 30 | |

| | |
|-----------------------------------------------------------------|--|
| Arg His Val Gly Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Arg Lys | |
| 35 40 45 | |

| | |
|-----------------------------------------------------------------|--|
| Lys Glu Met Asp Val Lys Glu Gly His Glu Ala Gly Phe Val Ser Met | |
| 50 55 60 | |

| | |
|-----------------------------------------------------------------|--|
| Ser Arg Ile Leu Glu Leu Cys Tyr Glu Ala Gly Val Asp Thr Ala Thr | |
| 65 70 75 80 | |

| | |
|-----------------------------------------------------------------|--|
| Val Phe Ala Phe Ser Ile Glu Asn Phe Lys Arg Ser Ser Arg Glu Val | |
| 85 90 95 | |

| | |
|-----------------------------------------------------------------|--|
| Glu Ser Leu Met Thr Leu Ala Arg Glu Arg Ile Arg Gln Ile Thr Glu | |
| 100 105 110 | |

| | |
|-----------------------------------------------------------------|--|
| Arg Gly Glu Leu Ala Cys Lys Tyr Gly Val Arg Ile Lys Ile Ile Gly | |
| 115 120 125 | |

| | |
|-----------------------------------------------------------------|--|
| Asp Leu Ser Leu Leu Asp Lys Ser Leu Leu Glu Asp Val Arg Val Ala | |
| 130 135 140 | |

| | |
|-----------------------------------------------------------------|--|
| Val Glu Thr Thr Lys Asn Asn Lys Arg Ala Thr Leu Asn Ile Cys Phe | |
| 145 150 155 160 | |

| | |
|-----------------------------------------------------------------|--|
| Pro Tyr Thr Gly Arg Glu Glu Ile Leu His Ala Met Lys Glu Thr Ile | |
|-----------------------------------------------------------------|--|

165

CL2039.ST25
170

175

Val Gln His Lys Lys Gly Ala Ala Ile Asp Glu Ser Thr Leu Glu Ser
 180 185 190

His Leu Tyr Thr Ala Gly Val Pro Pro Leu Asp Leu Leu Ile Arg Thr
 195 200 205

Ser Gly Val Ser Arg Leu Ser Asp Phe Leu Ile Trp Gln Ala Ser Ser
 210 215 220

Lys Gly Val Arg Ile Glu Leu Leu Asp Cys Leu Trp Pro Glu Phe Gly
 225 230 235 240

Pro Ile Arg Met Ala Trp Ile Leu Leu Lys Phe Ser Phe His Lys Ser
 245 250 255

Phe Leu Asn Lys Glu Tyr Arg Leu Glu Glu Gly Asp Tyr Asp Glu Glu
 260 265 270

Thr Asn Gly Asp Pro Ile Asp Leu Lys Glu Lys Lys Leu Asn
 275 280 285

<210> 21

<211> 1032

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 21
 atgaaaatgc ccagtattat tcagattcag tttgttagccc taaaaaggct tttggtagaa 60
 accaaagaac agatgtgctt cgcagtgaaa agtatatttc agagagtatt tgcgtgggtt 120
 atgtcattaa gcttgtttc atgggtttat gtaaaatcttc agaatatttt gataaaagca 180
 ttaaggtag ggccagtgcc tgaacatgtc tccttatca tggatggtaa ccggagatat 240
 gccaagtcaa gaaggctacc agtaaaaaaa ggccatgaag ctggtggtt aacgttacta 300
 acactactgt atatctgcaa aagattgggt gtaaaatgtg ttccgccta tgcattttct 360
 attgaaaatt ttaatagacc aaaagaagaa gtagatacgc taatgaattt gtttacggta 420
 aagctttagt aattcgcaaa aagagccaag gactataagg atcccttata cggatctaaa 480
 ataagaatag taggtgatca atctttacta tctccagaaa tgagaaaaaa aattaaaaaa 540
 gtggaagaaa tcacacagga tggagacgt ttcactttat ttatatgttt tccttacact 600
 tcaagaaatg atatgttaca tactattcgt gattcagttg aagaccattt ggaaaataaa 660
 tcaccaagga ttaatataag aaaatttact aataaaatgt acatgggtt ccattccat 720
 aatgtgaat tattaatcag aacaagtggg cataggaggc tctcagacta tatgctatgg 780

CL2039.ST25

| | |
|---------------------------------------------------------------------|------|
| caagtacatg aaaatgccac cattgaattt agtgatacgt tggccaaa ttttagcttc | 840 |
| tttgctatgt acctgatgtat tctcaaattgg tccttctttt ccaccattca aaaatataat | 900 |
| gagaagaatc actcattgtt tgaaaaata catgaaagcg ttcccttcaat atttaaaaaa | 960 |
| aagaaaaacag ctatgtcttt gtacaacttt ccaaaccccc ccatttcagt ttcggttaca | 1020 |
| ggagatgaat aa | 1032 |

<210> 22

<211> 343

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 22

| | |
|-----------------------------------------------------------------|--|
| Met Lys Met Pro Ser Ile Ile Gln Ile Gln Phe Val Ala Leu Lys Arg | |
| 1 5 10 15 | |

| | |
|-----------------------------------------------------------------|--|
| Leu Leu Val Glu Thr Lys Glu Gln Met Cys Phe Ala Val Lys Ser Ile | |
| 20 25 30 | |

| | |
|-----------------------------------------------------------------|--|
| Phe Gln Arg Val Phe Ala Trp Val Met Ser Leu Ser Leu Phe Ser Trp | |
| 35 40 45 | |

| | |
|-----------------------------------------------------------------|--|
| Phe Tyr Val Asn Leu Gln Asn Ile Leu Ile Lys Ala Leu Arg Val Gly | |
| 50 55 60 | |

| | |
|-----------------------------------------------------------------|--|
| Pro Val Pro Glu His Val Ser Phe Ile Met Asp Gly Asn Arg Arg Tyr | |
| 65 70 75 80 | |

| | |
|-----------------------------------------------------------------|--|
| Ala Lys Ser Arg Arg Leu Pro Val Lys Lys Gly His Glu Ala Gly Gly | |
| 85 90 95 | |

| | |
|-----------------------------------------------------------------|--|
| Leu Thr Leu Leu Thr Leu Leu Tyr Ile Cys Lys Arg Leu Gly Val Lys | |
| 100 105 110 | |

| | |
|-----------------------------------------------------------------|--|
| Cys Val Ser Ala Tyr Ala Phe Ser Ile Glu Asn Phe Asn Arg Pro Lys | |
| 115 120 125 | |

| | |
|-----------------------------------------------------------------|--|
| Glu Glu Val Asp Thr Leu Met Asn Leu Phe Thr Val Lys Leu Asp Glu | |
| 130 135 140 | |

| | |
|-----------------------------------------------------------------|--|
| Phe Ala Lys Arg Ala Lys Asp Tyr Lys Asp Pro Leu Tyr Gly Ser Lys | |
| 145 150 155 160 | |

| | |
|-----------------------------------------------------------------|--|
| Ile Arg Ile Val Gly Asp Gln Ser Leu Leu Ser Pro Glu Met Arg Lys | |
| 165 170 175 | |

CL2039.ST25

Lys Ile Lys Lys Val Glu Glu Ile Thr Gln Asp Gly Asp Asp Phe Thr
180 185 190

Leu Phe Ile Cys Phe Pro Tyr Thr Ser Arg Asn Asp Met Leu His Thr
195 200 205

Ile Arg Asp Ser Val Glu Asp His Leu Glu Asn Lys Ser Pro Arg Ile
210 215 220

Asn Ile Arg Lys Phe Thr Asn Lys Met Tyr Met Gly Phe His Ser Asn
225 230 235 240

Lys Cys Glu Leu Leu Ile Arg Thr Ser Gly His Arg Arg Leu Ser Asp
245 250 255

Tyr Met Leu Trp Gln Val His Glu Asn Ala Thr Ile Glu Phe Ser Asp
260 265 270

Thr Leu Trp Pro Asn Phe Ser Phe Phe Ala Met Tyr Leu Met Ile Leu
275 280 285

Lys Trp Ser Phe Phe Ser Thr Ile Gln Lys Tyr Asn Glu Lys Asn His
290 295 300

Ser Leu Phe Glu Lys Ile His Glu Ser Val Pro Ser Ile Phe Lys Lys
305 310 315 320

Lys Lys Thr Ala Met Ser Leu Tyr Asn Phe Pro Asn Pro Pro Ile Ser
325 330 335

Val Ser Val Thr Gly Asp Glu
340

<210> 23

<211> 271

<212> PRT

<213> *Arabidopsis*

<400> 23

Met Asn Thr Leu Glu Glu Val Asp Glu Ser Thr His Ile Phe Asn Ala
1 5 10 15

Leu Met Ser Leu Met Arg Lys Phe Leu Phe Arg Val Leu Cys Val Gly
20 25 30

Pro Ile Pro Thr Asn Ile Ser Phe Ile Met Asp Gly Asn Arg Arg Phe
35 40 45

CL2039.ST25

Ala Lys Lys His Asn Leu Ile Gly Leu Asp Ala Gly His Arg Ala Gly
50 55 60

Phe Ile Ser Val Lys Tyr Ile Leu Gln Tyr Cys Lys Glu Ile Gly Val
65 70 75 80

Pro Tyr Val Thr Leu His Ala Phe Gly Met Asp Asn Phe Lys Arg Gly
85 90 95

Pro Glu Glu Val Lys Cys Val Met Asp Leu Met Leu Glu Lys Val Glu
100 105 110

Leu Ala Ile Asp Gln Ala Val Ser Gly Asn Met Asn Gly Val Arg Ile
115 120 125

Ile Phe Ala Gly Asp Leu Asp Ser Leu Asn Glu His Phe Arg Ala Ala
130 135 140

Thr Lys Lys Leu Met Glu Leu Thr Glu Glu Asn Arg Asp Leu Ile Val
145 150 155 160

Val Val Cys Val Ala Tyr Ser Thr Ser Leu Glu Ile Val His Ala Val
165 170 175

Arg Lys Ser Cys Val Arg Lys Cys Thr Asn Gly Asp Asp Leu Val Leu
180 185 190

Leu Glu Leu Ser Asp Val Glu Glu Cys Met Tyr Thr Ser Ile Val Pro
195 200 205

Val Pro Asp Leu Val Ile Arg Thr Gly Gly Asp Arg Leu Ser Asn
210 215 220

Phe Met Thr Trp Gln Thr Ser Arg Ser Leu Leu His Arg Thr Glu Ala
225 230 235 240

Leu Trp Pro Glu Leu Gly Leu Trp His Leu Val Trp Ala Ile Leu Lys
245 250 255

Phe Gln Arg Met Gln Asp Tyr Leu Thr Lys Lys Lys Leu Asp
260 265 270

<210> 24

<211> 295

<212> PRT

<213> Arabidopsis

CL2039.ST25

<400> 24

Met Ala Glu Leu Pro Gly Gln Ile Arg His Ile Gly Gly Arg Met Ser
1 5 10 15Gln Leu Leu Glu Gln Ile Tyr Gly Phe Ser Arg Arg Ser Leu Phe Arg
20 25 30Val Ile Ser Met Gly Pro Ile Pro Cys His Ile Ala Phe Ile Met Asp
35 40 45Gly Asn Arg Arg Tyr Ala Lys Lys Cys Gly Leu Leu Asp Gly Ser Gly
50 55 60His Lys Ala Gly Phe Ser Ala Leu Met Ser Met Leu Gln Tyr Cys Tyr
65 70 75 80Glu Leu Gly Ile Lys Tyr Val Thr Ile Tyr Ala Phe Ser Ile Asp Asn
85 90 95Phe Arg Arg Lys Pro Glu Glu Val Glu Ser Val Met Asp Leu Met Leu
100 105 110Glu Lys Ile Lys Ser Leu Leu Glu Lys Glu Ser Ile Val His Gln Tyr
115 120 125Gly Ile Arg Val Tyr Phe Ile Gly Asn Leu Ala Leu Leu Asn Asp Gln
130 135 140Val Arg Ala Ala Ala Glu Lys Val Met Lys Ala Thr Ala Lys Asn Ser
145 150 155 160Arg Val Val Leu Leu Ile Cys Ile Ala Tyr Asn Ser Thr Asp Glu Ile
165 170 175Val Gln Ala Val Lys Lys Ser Cys Ile Asn Lys Ser Asp Asn Ile Glu
180 185 190Ala Ser Asn Tyr Lys His Glu Asp Ser Asp Ser Asp Ile Glu Gly Thr
195 200 205Asp Met Glu Asn Gln Glu Lys Lys Ile Gln Leu Val Asp Ile Glu Glu
210 215 220Asn Met Gln Met Ser Val Ala Pro Asn Pro Asp Ile Leu Ile Arg Ser
225 230 235 240Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Gly Asn
245 250 255

CL2039.ST25

Thr Gln Leu Cys Ser Pro Ala Ala Leu Trp Pro Glu Ile Gly Leu Arg
 260 265 270

His Leu Leu Trp Ala Ile Leu Asn Phe Gln Arg Asn His Ser Tyr Leu
 275 280 285

Glu Lys Arg Lys Lys Gln Leu
 290 295

<210> 25

<211> 303

<212> PRT

<213> *Arabidopsis*

<400> 25

Met Leu Ser Leu Leu Ser Ser Asp Ser Ser Leu Leu Ser Leu Leu Phe
 1 5 10 15

Leu Phe Leu Ile Pro Cys Leu Phe Ile Thr Ser Tyr Ile Gly Phe Pro
 20 25 30

Val Phe Leu Leu Lys Leu Ile Gly Leu Ile Lys Ile Lys Ala Ala Arg
 35 40 45

Asp Asn Glu Lys Arg Asp Glu Gly Thr Tyr Val Val Arg Glu Asp Gly
 50 55 60

Leu Gln Arg Glu Leu Met Pro Arg His Val Ala Phe Ile Leu Asp Gly
 65 70 75 80

Asn Arg Arg Trp Ala Lys Arg Ala Gly Leu Thr Thr Ser Gln Gly His
 85 90 95

Glu Ala Gly Ala Lys Arg Leu Ile Asp Ile Ala Glu Leu Cys Phe Glu
 100 105 110

Leu Gly Val His Thr Val Ser Ala Phe Ala Phe Ser Thr Glu Asn Trp
 115 120 125

Gly Arg Asp Lys Ile Glu Ile Asp Asn Leu Met Ser Leu Ile Gln His
 130 135 140

Tyr Arg Asn Lys Ser Asn Ile Lys Phe Phe His Arg Ser Glu Val Arg
 145 150 155 160

Val Ser Val Ile Gly Asn Lys Thr Lys Ile Pro Glu Ser Leu Leu Lys
 165 170 175

CL2039.ST25

Glu Ile His Glu Ile Glu Glu Ala Thr Lys Gly Tyr Lys Asn Lys His
180 185 190

Leu Ile Met Ala Val Asp Tyr Ser Gly Lys Phe Asp Ile Met His Ala
195 200 205

Cys Lys Ser Leu Val Lys Lys Ser Glu Lys Gly Leu Ile Arg Glu Glu
210 215 220

Asp Val Asp Glu Ala Leu Ile Glu Arg Glu Leu Leu Thr Asn Cys Ser
225 230 235 240

Asp Phe Pro Ser Pro Asp Leu Met Ile Arg Thr Ser Gly Glu Gln Arg
245 250 255

Ile Ser Asn Phe Phe Leu Trp Gln Leu Ala Tyr Ser Glu Leu Phe Phe
260 265 270

Ser Pro Val Phe Trp Pro Asp Phe Asp Lys Asp Lys Leu Leu Glu Ala
275 280 285

Leu Ala Ser Tyr Gln Arg Arg Glu Arg Arg Phe Gly Cys Arg Val
290 295 300

<210> 26

<211> 244

<212> PRT

<213> *Arabidopsis*

<400> 26

Met Gly Glu Lys Gln Lys Arg Gly Arg Asn Ile Met Pro Lys His Val
1 5 10 15

Ala Val Ile Leu Asp Gly Asn Arg Arg Trp Ala Glu Lys Arg Gly Leu
20 25 30

Gly Thr Ser Glu Gly His Glu Ala Gly Ala Arg Arg Leu Met Glu Asn
35 40 45

Ala Lys Asp Cys Phe Ala Met Gly Thr Asn Thr Ile Ser Leu Phe Ala
50 55 60

Phe Ser Thr Glu Asn Trp Glu Arg Pro Glu Asp Glu Val Lys Cys Leu
65 70 75 80

Met Ala Leu Phe Glu Lys Tyr Leu Ala Ser Asp Met Pro Tyr Leu Arg
85 90 95

CL2039.ST25

Ser Asp Lys Ile Lys Ile Ser Val Ile Gly Asn Arg Thr Lys Leu Pro
100 105 110

Glu Ser Leu Leu Gly Leu Ile Glu Glu Val Glu Glu Ala Thr Lys Ser
115 120 125

Tyr Glu Gly Lys Asn Leu Ile Ile Ala Ile Asp Tyr Ser Gly Arg Tyr
130 135 140

Asp Ile Leu Gln Ala Cys Lys Ser Leu Ala Asn Lys Val Lys Asp Gly
145 150 155 160

Leu Ile Gln Val Glu Asp Ile Asn Glu Lys Ala Met Glu Lys Glu Leu
165 170 175

Leu Thr Lys Cys Ser Glu Phe Pro Asn Pro Asp Leu Leu Ile Arg Thr
180 185 190

Ser Gly Glu Gln Arg Ile Ser Asn Phe Phe Leu Trp Gln Ser Ala Tyr
195 200 205

Thr Glu Leu Tyr Phe Pro Thr Val Leu Trp Pro Asp Phe Gly Glu Ala
210 215 220

Glu Tyr Leu Glu Ala Leu Thr Trp Tyr Gln Gln Arg Gln Arg Arg Phe
225 230 235 240

Gly Arg Arg Val

<210> 27

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Domain IV consensus sequence from Figure 1 alignment

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE
<222> (9)..(9)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (18)..(18)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> xaa = any amino acid

<400> 27

Tyr Ser Gly Arg Xaa Glu Ile Val Xaa Ala Val Lys Xaa Ser Xaa Xaa
1 5 10 15

Lys Xaa Xaa Xaa Gly
20

<210> 28

<211> 47

<212> PRT

<213> Artificial Sequence

<220>

<223> Domain v consensus sequence from Figure 1 alignment

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE
<222> (8)..(8)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (22)..(22)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (24)..(24)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (35)..(35)
<223> Xaa = any amino acid

<400> 28
Ile Xaa Xaa Xaa Glu Ile Xaa Xaa Xaa Leu Xaa Asp Xaa Glu Leu Xaa
1 5 10 15
Xaa Asn Xaa Xaa Xaa Xaa Pro Xaa Pro Asp Leu Leu Ile Arg Thr Ser
20 25 30
Gly Glu Xaa Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Ala Tyr
35 40 45

<210> 29

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence from Apfel CM et al. (J Bacteriol 1999 Jan;181 (2):483-492)

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (12)..(12)

<223> xaa = W or Y or F

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa = R or G

<400> 29

His Xaa Xaa Xaa Xaa Met Asp Gly Asn Xaa Arg Xaa Ala
1 5 10

<210> 30

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence from Apfel CM et al. (J Bacteriol 1999 Jan;181(2):483-492)

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa = any amino acid

<400> 30

Gly His Xaa Xaa Gly
1 5

<210> 31

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence from Apfel CM et al. (J Bacteriol 1999 Jan;181
Page 35

(2):483-492)

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa = T or S

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa = S or T

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (13)..(13)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (14)..(14)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (15)..(15)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (18)..(18)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (19)..(19)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (22)..(22)

<223> xaa = any amino acid

<400> 31

Xaa Xaa Xaa Ala Phe Ser Xaa Glu Asn Xaa Xaa Arg Xaa Xaa Xaa Glu
1 5 10 15

Val Xaa Xaa Leu Met Xaa Leu
20

<210> 32

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence from Apfel CM et al. (J Bacteriol 1999 Jan;181 (2):483-492)

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> xaa = D or E

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> xaa = L or I or V or M

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (12)..(12)

<223> Xaa = any amino acid

<400> 32

Ala Xaa Xaa Tyr Gly Gly Arg Xaa Xaa Xaa Xaa Xaa Ala
1 5 10

<210> 33

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence from Apfel CM et al. (J Bacteriol 1999 Jan;181 (2):483-492)

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa = D or E

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa = S or A or G

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa = M or L

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Xaa = L or M or P

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (23)..(23)
<223> Xaa = S or A or T

<220>
<221> MISC_FEATURE
<222> (25)..(25)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (26)..(26)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (28)..(28)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (31)..(31)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE

CL2039.ST25

<222> (34)..(34)

<223> Xaa = D or E

<400> 33

Xaa Leu Xaa Ile Arg Thr Xaa Gly Glu Xaa Arg Xaa Ser Asn Phe Xaa
1 5 10 15

Xaa Trp Gln Xaa Xaa Tyr Xaa Glu Xaa Xaa Phe Xaa Xaa Xaa Xaa Trp
20 25 30

Pro Xaa Phe
35

<210> 34

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence

<400> 34

Asp Ile Leu Val Arg Ser Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu
1 5 10 15

Leu Trp Gln Thr Thr Asn Cys Val Leu Tyr Ser Pro Lys Ala Leu Trp
20 25 30

Pro Glu Met
35

<210> 35

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial and non-naturally occurring peptide

<400> 35

Glu Leu Val Ile Ser Leu Ile Val Glu Ser
1 5 10

CL2039.ST25

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer NKH46
<400> 36
ttcgccggag ctccttacta a

21

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer NKH45
<400> 37
cgttcatgac ccgtatgctt tct

23

<210> 38
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence
<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa = L or M

<400> 38
Ala Phe Ile xaa Asp Gly Asn Arg Arg Phe Ala
1 5 10

<210> 39
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence
<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> xaa = T or S

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> xaa = D or E

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> xaa = any amino acid

<220>
<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa = any amino acid

<400> 39

Tyr Xaa Ser Xaa Xaa Xaa Ile Xaa Xaa Ala
1 5 10

<210> 40

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa = I or V

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa = I or V

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa = S or T

CL2039.ST25

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa = E or L

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa = S or T

<220>
<221> MISC_FEATURE
<222> (18)..(18)
<223> Xaa = any amino acid

<400> 40

Pro Xaa Pro Asp Xaa Leu Xaa Arg Xaa Ser Gly Xaa Xaa Arg Leu Ser
1 5 10 15

Asn Xaa Leu Leu Trp Gln
20

<210> 41
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer Dan5
<400> 41
ctcgacaatt tcaatcgacg cc 22

<210> 42
<211> 22
<212> DNA
<213> Artificial Sequence

CL2039.ST25

<220>

<223> Primer Dan6

<400> 42
gaaggaagtt gctcagcctt gt 22

<210> 43

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer DegHpts

<400> 43
atawtggatg gaaacmggag g 21

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer NKH5

<220>

<221> misc_feature

<222> (6)..(6)

<223> n = Inosine

<220>

<221> misc_feature

<222> (8)..(8)

<223> n = Inosine

<400> 44
tgccananh a dgwarttrct 20

<210> 45

CL2039.ST25

<211> 208

<212> PRT

<213> Taraxacum kok-saghyz

<400> 45

Leu Val Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Arg Lys Trp Asn
1 5 10 15Leu Thr Glu Gly Ala Gly His Lys Thr Gly Phe Leu Ala Leu Met Ser
20 25 30Val Leu Lys Tyr Cys Tyr Glu Ile Gly Val Lys Tyr Val Thr Ile Tyr
35 40 45Ala Phe Ser Leu Asp Asn Phe Asn Arg Arg Pro Asp Glu Val Gln Tyr
50 55 60Val Met Asp Leu Met Gln Asp Lys Ile Glu Gly Phe Leu Lys Glu Val
65 70 75 80Ser Ile Ile Asn Gln Tyr Gly Val Arg Val Leu Phe Ile Gly Asp Leu
85 90 95Asp Arg Leu Tyr Glu Pro Val Arg Ile Ala Ala Glu Lys Ala Met Glu
100 105 110Ala Thr Ala Lys Asn Ser Thr Thr Tyr Leu Leu Val Cys Val Ala Tyr
115 120 125Thr Ser Ser His Glu Ile Pro Arg Ala Ile His Glu Ala Cys Glu Glu
130 135 140Ser Ile Arg Val Met Asn Gly Asn Gly Phe Phe Asn Gly Ser Gly Tyr
145 150 155 160Thr Asn Val Asn His Gly Ser Gln Ala Val Ile Lys Val Val Asp Leu
165 170 175Asp Lys His Met Tyr Met Gly Val Ala Pro Asp Pro Asp Ile Leu Val
180 185 190Arg Ser Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp His Lys
195 200 205